

Supporting information file: Simulation results.

Table S1: **Cross-data-set survival prediction of the predictors derived from artificial data sets with 1000 correlated genes trained on the pooled data sets (normalized by Z-score normalization or ComBat).**

G=1000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	0.59	0.66	0.72	0.85	0.91	NA	0.78	0.57	0.56	0.59
DS2	0.72	NA	0.66	0.71	0.88	0.82	0.75	NA	0.52	0.55	0.68
DS3	0.70	0.65	NA	0.75	0.90	0.79	0.81	0.78	NA	0.60	0.67
DS4	0.60	0.60	0.64	NA	0.86	0.77	0.59	0.67	0.59	NA	0.75

AUCs ≥ 0.60 are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S2: Cross-data-set risk assessment of the predictors derived from artificial data sets with 1000 correlated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).

G=1000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	p>0.05	1.79 (1.13-2.84) p=0.01	p>0.05	6.85 (3.94-11.91) p=9.88e-12	6.21 (3.56-10.83) p=1.27e-10	NA	4.75 (2.69-8.37) p=7.25e-08	p>0.05	p>0.05	p>0.05
DS2	2.44 (1.48-4.03) p=0.0004	NA	2.25 (1.39-3.64) p=0.0009	2.52 (1.56-4.07) p=0.0001	6.88 (3.80-12.43) p=1.71e-10	5.62 (2.99-10.58) p=8.33e-08	4.13 (2.23-7.65) p=6.12e-06	NA	p>0.05	p>0.05	3.24 (1.99-5.28) p=2.37e-06
DS3	p>0.05	1.77 (1.05-2.97) p=0.03	NA	2.52 (1.47-4.30) p=0.0007	4.99 (2.90-8.61) p=7.28e-09	3.38 (1.94-5.89) p=1.68e-05	4.24 (2.31-7.78) p=3.14e-06	3.54 (1.94-6.47) p=3.96e-05	NA	1.77 (1.02-3.07) p=0.04	2.24 (1.27-3.94) p=0.005
DS4	p>0.05	1.84 (1.08-3.15) p=0.02	2.40 (1.38-4.16) p=0.001	NA	4.61 (2.56-8.29) p=3.49e-07	2.60 (1.51-4.46) p=0.0005	p>0.05	2.91 (1.61-5.25) p=0.0003	p>0.05	NA	3.26 (1.85-5.75) p=4.13e-05

The HRs with $p \leq 0.05$ are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S3: Cross-data-set survival prediction of the predictors derived from artificial data sets with 5000 correlated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).

G=5000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	0.69	0.69	0.62	0.83	0.88	NA	0.59	0.57	0.56	0.59
DS2	0.60	NA	0.73	0.46	0.85	0.85	0.52	NA	0.52	0.41	0.63
DS3	0.60	0.69	NA	0.56	0.86	0.73	0.65	0.59	NA	0.59	0.54
DS4	0.52	0.62	0.53	NA	0.84	0.72	0.52	0.58	0.52	NA	0.66

AUCs ≥ 0.60 are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S4: **Cross-data-set performance of the predictors derived from artificial data sets with 5000 correlated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).**

G=5000												
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*		DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	2.31 (1.44-3.68) p=0.0004	1.97 (1.24-3.14) p=0.004	2.03 (1.28-3.23) p=0.002	4.84 (2.89-8.12) p=2.21e-09	6.48 (3.57-11.76) p=7.67e-10		NA	p>0.05	p>0.05	p>0.05	p>0.05
DS2	p>0.05	NA	2.15 (1.29-3.59) p=0.003	p>0.05	6.08 (3.54-10.42) p=5.39e-11	5.44 (3.01-9.83) p=1.97e-08		p>0.05	NA	p>0.05	p>0.05	1.76 (1.10-2.80) p=0.01
DS3	p>0.05	1.65 (1.00-2.71) p=0.048	NA	p>0.05	7.59 (4.00-14.42) p=6.01e-10	2.92 (1.63-5.22) p=0.0003		p>0.05	p>0.05	NA	p>0.05	p>0.05
DS4	p>0.05	p>0.05	1.78 (1.00-3.16) p=0.04	NA	6.51 (3.45-12.27) p=7.045e-09	2.53 (1.40-4.56) p=0.002		p>0.05	p>0.05	p>0.05	NA	1.68 (1.01-2.80) p=0.04

The HRs with $p \leq 0.05$ are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S5: **Cross-data-set survival prediction of the predictors derived from artificial data sets with 1000 uncorrelated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).**

G=1000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	0.86	0.64	0.72	0.88	0.91	NA	0.82	0.63	0.72	0.89
DS2	0.81	NA	0.69	0.71	0.88	0.82	0.81	NA	0.68	0.72	0.88
DS3	0.76	0.72	NA	0.60	0.92	0.76	0.77	0.66	NA	0.61	0.93
DS4	0.71	0.71	0.64	NA	0.84	0.77	0.70	0.67	0.64	NA	0.84

AUCs ≥ 0.60 are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S6: **Cross-data-set risk-assessment of the predictors derived from artificial data sets with 1000 uncorrelated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).**

G=1000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	5.06 (2.99-8.58) p=1.65e-09	2.05 (1.26-3.33) p=0.003	2.78 (1.68-4.60) p=7.14e-05	6.12 (3.49-10.74) p=2.67e-10	13.77 (7.11-26.65) p=7.21e-15	NA	4.10 (2.44-6.87) p=8.67e-08	2.11 (1.30-3.44) p=0.002	3.02 (1.79-5.08) p=3.17e-05	6.12 (3.49-10.74) p=2.67e-10
DS2	4.01 (2.38-6.78) p=2.01e-07	NA	2.08 (1.30-3.35) p=0.002	2.25 (1.41-3.59) p=0.0006	7.48 (4.20-13.34) p=8.91e-12	5.91 (3.22-10.84) p=9.74e-09	4.01 (2.38-6.78) p=2.01e-07	NA	1.79 (1.12-2.86) p=0.01	2.11 (1.32-3.37) p=0.001	7.60 (4.23-13.66) p=1.26e-11
DS3	2.53 (1.49-4.31) p=0.0005	2.57 (1.54-4.29) p=0.0002	NA	p>0.05	6.67 (4.00-11.12) p=3.82e-13	3.57 (2.12-5.99) p=1.57e-06	2.81 (1.65-4.78) p=0.0001	2.38 (1.41-4.01) p=0.001	NA	p>0.05	6.67 (4.00-11.12) p=3.82e-13
DS4	3.33 (1.95-5.70) p=1.09e-05	3.50 (2.08-5.91) p=2.65e-06	1.95 (1.20-3.17) p=0.006	NA	5.85 (3.10-11.06) p=5.21e-08	3.35 (2.00-5.61) p=4.03e-06	3.08 (1.81-5.23) p=3.17e-05	2.23 (1.38-3.61) p=0.001	1.94 (1.20-3.15) p=0.007	NA	5.85 (3.10-11.06) p=5.21e-08

The HRs with $p \leq 0.05$ are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S7: **Cross-data-set survival prediction of the predictors derived from artificial data sets with 5000 uncorrelated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).**

G=5000											
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*	DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	0.80	0.61	0.59	0.79	0.88	NA	0.80	0.63	0.56	0.79
DS2	0.66	NA	0.49	0.46	0.91	0.81	0.66	NA	0.52	0.46	0.92
DS3	0.68	0.67	NA	0.40	0.88	0.75	0.67	0.67	NA	0.40	0.88
DS4	0.61	0.73	0.50	NA	0.79	0.78	0.62	0.73	0.57	NA	0.78

AUCs ≥ 0.60 are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.

Table S8: Cross-data-set risk assessment of the predictors derived from artificial data sets with 5000 uncorrelated genes trained on the combined data sets (normalized by Z-score normalization or ComBat).

G=5000												
	DS1	DS2	DS3	DS4	Merged-zscore1*	Merged-zscore2*		DS1	DS2	DS3	DS4	Merged-combat*
DS1	NA	3.21 (1.94-5.30) p=5.48e-06	p>0.05	p>0.05	3.70 (2.18-6.27) p=1.12e-06	4.01 (2.33-6.89) p=5.15e-07		NA	3.21 (1.94-5.30) p=5.48e-06	p>0.05	1.96 (1.20-3.22) p=0.007	3.70 (2.18-6.27) p=1.12e-06
DS2	2.15 (1.30-3.53) p=0.002	NA	p>0.05	0.55 (0.33-0.93) p=0.02	6.89 (3.97-11.95) p=6.93e-12	10.86 (4.95-23.83) p=2.66e-09		2.17 (1.32-3.59) p=0.002	NA	p>0.05	0.59 (0.35-1.00) p=0.04	6.89 (3.97-11.95) p=6.93e-12
DS3	3.87 (2.08-7.20) p=1.92e-05	2.29 (1.28-4.11) p=0.005	NA	0.51 (0.29-0.91) p=0.02	6.62 (3.73-11.76) p=1.11e-10	5.10 (2.74-9.49) p=2.81e-07		3.87 (2.08-7.20) p=1.92e-05	2.29 (1.28-4.11) p=0.005	NA	0.51 (0.29-0.91) p=0.02	6.62 (3.73-11.76) p=1.11e-10
DS4	2.02 (1.16-3.53) p=0.01	2.26 (1.30-3.95) p=0.004	p>0.05	NA	3.94 (2.13-7.30) p=1.26e-05	5.84 (3.04-11.24) p=1.25e-07		2.15 (1.23-3.76) p=0.007	2.26 (1.29-3.94) p=0.004	p>0.05	NA	3.94 (2.13-7.30) p=1.26e-05

The HRs with $p \leq 0.05$ are significant. Merged-zscore1 refers to the merged data set combined from the individual data sets, each normalized separately by Z-score normalization. Merged-zscore2 refers to the separate Z-score normalization of the training set (merged data set) and the testing set. The training sets are listed in the column header and the testing sets are indicated in the row header of the table. * indicates that the predictor was trained from all data sets except the testing set. G stands for the number of genes. NA stands for Not Available.